

Andreas-David Brunner

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19
papers

892
citations

12
h-index

25
g-index

25
ext. papers

1,756
ext. citations

17.4
avg, IF

4.24
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 19 | Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation.. <i>Molecular Systems Biology</i> , 2022 , 18, e10798 | 12.2 | 24 |
| 18 | OpenCell: Endogenous tagging for the cartography of human cellular organization.. <i>Science</i> , 2022 , 375, eabi6983 | 33.3 | 9 |
| 17 | The Swiss Primary Hypersomnolence and Narcolepsy Cohort study (SPHYNCS): Study protocol for a prospective, multicentre cohort observational study. <i>Journal of Sleep Research</i> , 2021 , 30, e13296 | 5.8 | 3 |
| 16 | Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. <i>Nature Metabolism</i> , 2021 , 3, 1017-1031 | 14.6 | 13 |
| 15 | Deep learning the collisional cross sections of the peptide universe from a million experimental values. <i>Nature Communications</i> , 2021 , 12, 1185 | 17.4 | 21 |
| 14 | Reply to "Quality control requirements for the correct annotation of lipidomics data". <i>Nature Communications</i> , 2021 , 12, 4772 | 17.4 | 1 |
| 13 | AlphaMap: an open-source python package for the visual annotation of proteomics data with sequence specific knowledge. <i>Bioinformatics</i> , 2021 , | 7.2 | 3 |
| 12 | Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020 , 367, 1140-1146 | 33.6 | 168 |
| 11 | Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020 , 11, 331 | 17.4 | 78 |
| 10 | diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020 , 17, 1229-1236 | 21.6 | 85 |
| 9 | MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 982-994 | 7.6 | 54 |
| 8 | Site-specific ubiquitylation and SUMOylation using genetic-code expansion and sortase. <i>Nature Chemical Biology</i> , 2019 , 15, 276-284 | 11.7 | 55 |
| 7 | Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2534-2545 | 7.6 | 280 |
| 6 | Deep learning the collisional cross sections of the peptide universe from a million training samples | | 2 |
| 5 | Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation | | 46 |
| 4 | Parallel accumulation Serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage | | 18 |
| 3 | OpenCell: proteome-scale endogenous tagging enables the cartography of human cellular organization | | 4 |

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| 2 | AI-driven Deep Visual Proteomics defines cell identity and heterogeneity | 12 |
| 1 | AlphaMap: An open-source Python package for the visual annotation of proteomics data with sequence specific knowledge | 1 |